SEQUENCE LISTING

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WAGNER, Claudia
STEVANOVIC, Stephan
PFREUNDSCHUH, Michael

<120> SSX-2 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

<130> L0461.70158US00

<150> US 09/408,036
<151> 1999-09-29

<160> 51

<170> PatentIn version 3.2

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gac gac gcc ttt gca agg aga ccc acg gtt ggt gct caa ata cca gag 165
Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln Ile Pro Glu
5 10 15

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20 25 30 35

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Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met
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Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln Gly Asn Asp
70 75 80

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Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg Pro Gln Met
85 90 95

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act ttc ggc agg ctc cag gga atc tcc ccg aag atc atg ccc aag aag      453
Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met Pro Lys Lys
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cca gca gag gaa gga aat gat tcg gag gaa gtg cca gaa gca tct ggc      501
Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly
                120                 125                 130

cca caa aat gat ggg aaa gag ctg tgc ccc ccg gga aaa cca act acc      549
Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr
            135                 140                 145

tct gag aag att cac gag aga tct gga ccc aaa agg ggg gaa cat gcc      597
Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly Glu His Ala
        150                 155                 160

tgg acc cac aga ctg cgt gag aga aaa cag ctg gtg att tat gaa gag      645
Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu
    165                 170                 175

atc agc gac cct gag gaa gat gac gag taa ctcccctcag ggatacgaca       695
Ile Ser Asp Pro Glu Glu Asp Asp Glu
180                 185

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cacacacaca cacacacaca cacacacaca cacaccaagt accagtataa gcatctgcca   1175

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catgtactcc cctcatccga ttcccctgta gcagtcactg acagttaata aacctttgca   1295

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Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
            20                  25                  30
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Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
        35                  40                  45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
    50                  55                  60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65                  70                  75                  80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
                85                  90                  95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
            100                 105                 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
        115                 120                 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
    130                 135                 140

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
145                 150                 155                 160

Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
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Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
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gac gac gcc ttt gca agg aga ccc acg gtt ggt gct caa ata cca gag       165
Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln Ile Pro Glu
    5                   10                  15

aag atc caa aag gcc ttc gat gat att gcc aaa tac ttc tct aag gaa       213
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Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe Ser Lys Glu
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Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met
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aag aga aag tat gag gct atg act aaa cta ggt ttc aag gcc acc ctc      309
Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys Ala Thr Leu
            55                  60                  65

cca cct ttc atg tgt aat aaa cgg gcc gaa gac ttc cag ggg aat gat      357
Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln Gly Asn Asp
        70                  75                  80

ttg gat aat gac cct aac cgt ggg aat cag gtt gaa cgt cct cag atg      405
Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg Pro Gln Met
    85                  90                  95

act ttc ggc agg ctc cag gga atc tcc ccg aag atc atg ccc aag aag      453
Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met Pro Lys Lys
100                 105                 110                 115

cca gca gag gaa gga aat gat tcg gag gaa gtg cca gaa gca tct ggc      501
Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly
                120                 125                 130

cca caa aat gat ggg aaa gag ctg tgc ccc ccg gga aaa cca act acc      549
Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr
            135                 140                 145

tct gag aag att cac gag aga tct gga aat agg gag gcc caa gaa aag      597
Ser Glu Lys Ile His Glu Arg Ser Gly Asn Arg Glu Ala Gln Glu Lys
        150                 155                 160

gaa gag aga cgc gga aca gct cat cgg tgg agc agt cag aac aca cac      645
Glu Glu Arg Arg Gly Thr Ala His Arg Trp Ser Ser Gln Asn Thr His
    165                 170                 175

aac att ggt cga ttc agt ttg tca act tct atg ggt gca gtt cat ggt      693
Asn Ile Gly Arg Phe Ser Leu Ser Thr Ser Met Gly Ala Val His Gly
180                 185                 190                 195

acc ccc aaa aca att aca cac aac agg gac cca aaa ggg ggg aac atg      741
Thr Pro Lys Thr Ile Thr His Asn Arg Asp Pro Lys Gly Gly Asn Met
                200                 205                 210

cct gga ccc aca gac tgc gtg aga gaa aac agc tgg tga tttatgaaga       790
Pro Gly Pro Thr Asp Cys Val Arg Glu Asn Ser Trp
            215                 220

gatcagcgac cctgaggaag atgacgagta actcccctca gggatacgac acatgcccat    850

gatgagaagc agaacgtggt gacctttcac gaacatgggc atggctgcgg acccctcgtc    910

atcaggtgca tagcaagtga aagcaagtgt tcacaacagt gaaaagttga gcgtcatttt    970

tcttagtgtg ccaagagttc gatgttagcg tttacgttgt attttcttac actgtgtcat   1030

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acacacacac acacacacac acacaccaag taccagtata agcatctgcc atctgctttt 1330

cccattgcca tgcgtcctgg tcaagctccc ctcactctgt ttcctggtca gcatgtactc 1390

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aaaaaaaaaa aaaaaa 1466

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Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
35 40 45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
50 55 60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65 70 75 80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
85 90 95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
100 105 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
115 120 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
130 135 140

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Asn Arg Glu Ala
145 150 155 160

Gln Glu Lys Glu Glu Arg Arg Gly Thr Ala His Arg Trp Ser Ser Gln

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                165                 170                 175

Asn Thr His Asn Ile Gly Arg Phe Ser Leu Ser Thr Ser Met Gly Ala
            180                 185                 190

Val His Gly Thr Pro Lys Thr Ile Thr His Asn Arg Asp Pro Lys Gly
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Gly Asn Met Pro Gly Pro Thr Asp Cys Val Arg Glu Asn Ser Trp
    210                 215                 220


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                                    Met Asn Gly Asp Asp Ala Phe
                                    1               5

gca agg aga ccc acg gtt ggt gct caa ata cca gag aag atc caa aag     162
Ala Arg Arg Pro Thr Val Gly Ala Gln Ile Pro Glu Lys Ile Gln Lys
        10                  15                  20

gcc ttc gat gat att gcc aaa tac ttc tct aag gaa gag tgg gaa aag     210
Ala Phe Asp Asp Ile Ala Lys Tyr Phe Ser Lys Glu Glu Trp Glu Lys
    25                  30                  35

atg aaa gcc tcg gag aaa atc ttc tat gtg tat atg aag aga aag tat     258
Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys Tyr
40                  45                  50                  55

gag gct atg act aaa cta ggt ttc aag gcc acc ctc cca cct ttc atg     306
Glu Ala Met Thr Lys Leu Gly Phe Lys Ala Thr Leu Pro Pro Phe Met
                60                  65                  70

tgt aat aaa cgg gcc gaa gac ttc cag ggg aat gat ttg gat aat gac     354
Cys Asn Lys Arg Ala Glu Asp Phe Gln Gly Asn Asp Leu Asp Asn Asp
            75                  80                  85

cct aac cgt ggg aat cag gtt gaa cgt cct cag atg act ttc ggc agg     402
Pro Asn Arg Gly Asn Gln Val Glu Arg Pro Gln Met Thr Phe Gly Arg
        90                  95                  100

ctc cag gga atc tcc ccg aag atc atg ccc aag aag cca gca gag gaa     450
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Leu Gln Gly Ile Ser Pro Lys Ile Met Pro Lys Lys Pro Ala Glu Glu
    105                 110                 115

gga aat gat tcg gag gaa gtg cca gaa gca tct ggc cca caa aat gat      498
Gly Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly Pro Gln Asn Asp
120                 125                 130                 135

ggg aaa gag ctg tgc ccc ccg gga aaa cca act acc tct gag aag att      546
Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr Ser Glu Lys Ile
                140                 145                 150

nnn nnn nnn nnn nng acc caa aag ggg gga aca tgc ctg gac cca cag      594
Xaa Xaa Xaa Xaa Xaa Thr Gln Lys Gly Gly Thr Cys Leu Asp Pro Gln
            155                 160                 165

act gcg tga gagaaaacag ctggtgattt atgaagagat cagcgaccct              643
Thr Ala

gaggaagatg acgagtaact cccctcgggg atacgacaca tgcccatgat gagaagtaga    703

acgtggtgac ctttcacgaa cataggcatg gctgcggacc cctcgtcatc aggtgcatag    763

caagtgaaag caagtgttca caacagtgaa aagttgagcg tcgtttttct tagtgtgaca    823

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agcgttttca ttgatgagca agacatgctt aatgtgtatt tcggtttgtg tatccatgca    943

cctacctcag aaagcaagta tagtcaggta ttctctccat agaacagcac taccctcctc   1003

tctccccaga tgtgactact gagggcagat ctgagtgttt aatttccgat tttcccctct   1063

gcatttacac accagacaca caaacacaca cacacagaca cacacacaca cagacacacc   1123

aagtaccagt ataagcatct cccatatgct tttccccatt gccatgagtc ctggtcaagc   1183

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<213> Homo sapiens

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<222> (152)..(152)
<223> The 'Xaa' at location 152 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

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<222> (153)..(153)
<223> The 'Xaa' at location 153 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>

<221> misc_feature
<222> (154)..(154)
<223> The 'Xaa' at location 154 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
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<222> (155)..(155)
<223> The 'Xaa' at location 155 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
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<222> (156)..(156)
<223> The 'Xaa' at location 156 stands for Lys, Arg, Thr, Met, Glu, Gly, Ala, Val, Gln, Pro, Leu, Trp, or Ser.

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Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln
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Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
            20                  25                  30

Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
        35                  40                  45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
    50                  55                  60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65                  70                  75                  80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
                85                  90                  95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
            100                 105                 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
        115                 120                 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
    130                 135                 140

Pro Thr Thr Ser Glu Lys Ile Xaa Xaa Xaa Xaa Xaa Thr Gln Lys Gly
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Gly Thr Cys Leu Asp Pro Gln Thr Ala
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<400> 7

Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln
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Ile Pro Glu Lys Ile Gln
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Ala Lys Tyr Phe Ser Lys
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<210> 9
<211> 22
<212> PRT
<213> Homo sapiens

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Phe Asp Asp Ile Ala Lys Tyr Phe Ser Lys Glu Glu Trp Glu Lys Met
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Lys Ala Ser Glu Lys Ile
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<210> 10
<211> 22
<212> PRT
<213> Homo sapiens

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Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys
1 5 10 15

Arg Lys Tyr Glu Ala Met
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<212> PRT
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Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
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Ala Thr Leu Pro Pro Phe
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<212> PRT
<213> Homo sapiens

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Leu Gly Phe Lys Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala
1 5 10 15

Glu Asp Phe Gln Gly Asn
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<212> PRT
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<400> 13

Asn Lys Arg Ala Glu Asp Phe Gln Gly Asn Asp Leu Asp Asn Asp Pro
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Asn Arg Gly Asn Gln Val
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<210> 14
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Asp Pro Asn Arg Gly Asn Gln Val Glu Arg Pro Gln Met Thr Phe Gly
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Arg Leu Gln

<210> 15

<211> 22
<212> PRT
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<400> 15

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
1 5 10 15

Pro Lys Lys Pro Ala Glu
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<210> 16
<211> 22
<212> PRT
<213> Homo sapiens

<400> 16

Pro Lys Ile Met Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu
1 5 10 15

Glu Val Pro Glu Ala Ser
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<210> 17
<211> 22
<212> PRT
<213> Homo sapiens

<400> 17

Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly Pro Gln Asn Asp Gly
1 5 10 15

Lys Glu Leu Cys Pro Pro
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<212> PRT
<213> Homo sapiens

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Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr Ser
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Glu Lys Ile His Glu Arg
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<210> 19
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<213> Homo sapiens

<400> 19

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
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Glu His Ala Trp Thr His
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<210> 20
<211> 22
<212> PRT
<213> Homo sapiens

<400> 20

Pro Lys Arg Gly Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys
1 5 10 15

Gln Leu Val Ile Tyr Glu
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<210> 21
<211> 20
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Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu Ile Ser Asp Pro Glu
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Glu Asp Asp Glu
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<210> 22
<211> 20
<212> PRT
<213> Homo sapiens

<400> 22

Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys
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Tyr Glu Ala Met
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<212> PRT
<213> Homo sapiens

<400> 23

Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys Tyr Glu
1 5 10 15

Ala Met

<210> 24
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<212> PRT
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<400> 24

Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys Tyr Glu Ala Met
1 5 10 15

<210> 25
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<212> PRT
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<400> 25

Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys Tyr Glu Ala Met
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<400> 26

Phe Tyr Val Tyr Met Lys Arg Lys Tyr Glu Ala Met
1 5 10

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<212> PRT
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<400> 27

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met
1 5 10

<210> 28
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<400> 28

Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys

1 5 10 15

Arg Lys Tyr Glu
20

<210> 29
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<400> 29

Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys
1 5 10 15

Arg Lys

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Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys
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1 5 10

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Lys Ile Val Tyr Val Tyr Met Lys Arg Lys Tyr Glu Ala Met
1 5 10

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Lys Ile Ser Tyr Val Tyr Met Lys Arg Asn Tyr Lys Ala Met
1 5 10

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Lys Ile Val Tyr Val Tyr Met Lys Leu Asn Tyr Glu Val Met
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Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
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<210> 42
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<400> 42

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1 5 10 15

<210> 43
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<212> PRT
<213> Homo sapiens

<400> 43

Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met Pro Lys Lys
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<212> PRT
<213> Homo sapiens

<400> 44

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